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SEQUENCE LISTING

<110> The Scripps Research Institute
      The Regents of the University of California
      Wu, Eugene
      Nemerow, Glen R.
      Stewart, Phoebe

<120> MODIFIED FIBER PROTEINS FOR EFFICIENT
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<151 2003-06-11

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gcaggaccac ttctgcgctc ggcccttccg gctggctggt ttattgctga taaatctgga 9960
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<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 25
tgtacaccgg atccggcgca cacc   24

<210> 26
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 26
cacaacgagc tcaattaatt aattgccaca tcctc   35

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 27

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cgcgctgact cttaaggact agtttc                              26

<210> 28
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 28
gcgcttaatt aacatcatca ataatatacc ttattttt                37

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 29
atcatggccg acaagcagaa gaac                               24

<210> 30
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 30
gtacagctcg tccatgccga gagt                               24

<210> 31
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> EGFP probe

<221> misc_feature
<222> 1
<223> FAM (6-carboxy-fluorescein)

<221> misc_feature
<222> 26
<223> TAMRA (6-carboxy-tetramethyl-rhodamine)

<400> 31
caggaccatg tgatcgcgct tctcgt                             26

<210> 32
<211> 1749
<212> DNA
<213> Adenovirus serotype 2 fiber

<220>
<221> CDS
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<222> (1)...(1749)

<400> 32
atg aaa cgc gcc aga ccg tct gaa gac acc ttc aac ccc gtg tat cca    48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5                   10                  15

tat gac aca gaa acc ggg cct cca act gtg ccc ttt ctt acc cct cca    96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30

ttt gtt tca ccc aat ggt ttc caa gaa agt ccc cct gga gtt ctc tct   144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45

cta cgc gtc tcc gaa cct ttg gac acc tcc cac ggc atg ctt gcg ctt   192
Leu Arg Val Ser Glu Pro Leu Asp Thr Ser His Gly Met Leu Ala Leu
    50                  55                  60

aaa atg ggc agc ggt ctt acc cta gac aag gcc gga aac ctc acc tcc   240
Lys Met Gly Ser Gly Leu Thr Leu Asp Lys Ala Gly Asn Leu Thr Ser
65                  70                  75                  80

caa aat gta acc act gtt act cag cca ctt aaa aaa aca aag tca aac   288
Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95

ata agt ttg gac acc tcc gca cca ctt aca att acc tca ggc gcc cta   336
Ile Ser Leu Asp Thr Ser Ala Pro Leu Thr Ile Thr Ser Gly Ala Leu
            100                 105                 110

aca gtg gca acc acc gct cct ctg ata gtt act agc ggc gct ctt agc   384
Thr Val Ala Thr Thr Ala Pro Leu Ile Val Thr Ser Gly Ala Leu Ser
        115                 120                 125

gta cag tca caa gcc cca ctg acc gtg caa gac tcc aaa cta agc att   432
Val Gln Ser Gln Ala Pro Leu Thr Val Gln Asp Ser Lys Leu Ser Ile
    130                 135                 140

gct act aaa ggg ccc att aca gtg tca gat gga aag cta gcc ctg caa   480
Ala Thr Lys Gly Pro Ile Thr Val Ser Asp Gly Lys Leu Ala Leu Gln
145                 150                 155                 160

aca tca gcc ccc ctc tct ggc agt gac agc gac acc ctt act gta act   528
Thr Ser Ala Pro Leu Ser Gly Ser Asp Ser Asp Thr Leu Thr Val Thr
                165                 170                 175

gca tca ccc ccg cta act act gcc acg ggt agc ttg ggc att aac atg   576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asn Met
            180                 185                 190

gaa gat cct att tat gta aat aat gga aaa ata gga att aaa ata agc   624
Glu Asp Pro Ile Tyr Val Asn Asn Gly Lys Ile Gly Ile Lys Ile Ser
        195                 200                 205

ggt cct ttg caa gta gca caa aac tcc gat aca cta aca gta gtt act   672
Gly Pro Leu Gln Val Ala Gln Asn Ser Asp Thr Leu Thr Val Val Thr
    210                 215                 220

gga cca ggt gtc acc gtt gaa caa aac tcc ctt aga acc aaa gtt gca   720
Gly Pro Gly Val Thr Val Glu Gln Asn Ser Leu Arg Thr Lys Val Ala
225                 230                 235                 240
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      225                        230                         235                          240

gga gct att ggt tat gat tca tca aac aac atg gaa att aaa acg ggc          768
Gly Ala Ile Gly Tyr Asp Ser Ser Asn Asn Met Glu Ile Lys Thr Gly
                    245             250                 255

ggt ggc atg cgt ata aat aac aac ttg tta att cta gat gtg gat tac          816
Gly Gly Met Arg Ile Asn Asn Asn Leu Leu Ile Leu Asp Val Asp Tyr
            260             265                 270

cca ttt gat gct caa aca aaa cta cgt ctt aaa ctg ggg cag gga ccc          864
Pro Phe Asp Ala Gln Thr Lys Leu Arg Leu Lys Leu Gly Gln Gly Pro
        275             280                 285

ctg tat att aat gca tct cat aac ttg gac ata aac tat aac aga ggc          912
Leu Tyr Ile Asn Ala Ser His Asn Leu Asp Ile Asn Tyr Asn Arg Gly
    290             295                 300

cta tac ctt ttt aat gca tca aac aat act aaa aaa ctg gaa gtt agc          960
Leu Tyr Leu Phe Asn Ala Ser Asn Asn Thr Lys Lys Leu Glu Val Ser
305             310                 315                 320

ata aaa aaa tcc agt gga cta aac ttt gat aat act gcc ata gct ata         1008
Ile Lys Lys Ser Ser Gly Leu Asn Phe Asp Asn Thr Ala Ile Ala Ile
                325             330                 335

aat gca gga aag ggt ctg gag ttt gat aca aac aca tct gag tct cca         1056
Asn Ala Gly Lys Gly Leu Glu Phe Asp Thr Asn Thr Ser Glu Ser Pro
            340             345                 350

gat atc aac cca ata aaa act aaa att ggc tct ggc att gat tac aat         1104
Asp Ile Asn Pro Ile Lys Thr Lys Ile Gly Ser Gly Ile Asp Tyr Asn
        355             360                 365

gaa aac ggt gcc atg att act aaa ctt gga gcg ggt tta agc ttt gac         1152
Glu Asn Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp
370             375                 380

aac tca ggg gcc att aca ata gga aac aaa aat gat gac aaa ctt acc         1200
Asn Ser Gly Ala Ile Thr Ile Gly Asn Lys Asn Asp Asp Lys Leu Thr
385             390                 395                 400

ctg tgg aca acc cca gac cca tct cct aac tgc aga att cat tca gat         1248
Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile His Ser Asp
                405             410                 415

aat gac tgc aaa ttt act ttg gtt ctt aca aaa tgt ggg agt caa gta         1296
Asn Asp Cys Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val
            420             425                 430

cta gct act gta gct gct ttg gct gta tct gga gat ctt tca tcc atg         1344
Leu Ala Thr Val Ala Ala Leu Ala Val Ser Gly Asp Leu Ser Ser Met
        435             440                 445

aca ggc acc gtt gca agt gtt agt ata ttc ctt aga ttt gac caa aac         1392
Thr Gly Thr Val Ala Ser Val Ser Ile Phe Leu Arg Phe Asp Gln Asn
    450             455                 460

ggt gtt cta atg gag aac tcc tca ctt aaa aaa cat tac tgg aac ttt         1440
Gly Val Leu Met Glu Asn Ser Ser Leu Lys Lys His Tyr Trp Asn Phe
465             470                 475                 480
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aga aat ggg aac tca act aat gca aat cca tac aca aat gca gtt gga    1488
Arg Asn Gly Asn Ser Thr Asn Ala Asn Pro Tyr Thr Asn Ala Val Gly
            485             490                 495

ttt atg cct aac ctt cta gcc tat cca aaa acc caa agt caa act gct    1536
Phe Met Pro Asn Leu Leu Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala
            500             505                 510

aaa aat aac att gtc agt caa gtt tac ttg cat ggt gat aaa act aaa    1584
Lys Asn Asn Ile Val Ser Gln Val Tyr Leu His Gly Asp Lys Thr Lys
            515             520                 525

cct atg ata ctt acc att aca ctt aat ggc act agt gaa tcc aca gaa    1632
Pro Met Ile Leu Thr Ile Thr Leu Asn Gly Thr Ser Glu Ser Thr Glu
            530             535                 540

act agc gag gta agc act tac tct atg tct ttt aca tgg tcc tgg gaa    1680
Thr Ser Glu Val Ser Thr Tyr Ser Met Ser Phe Thr Trp Ser Trp Glu
545             550                 555                 560

agt gga aaa tac acc act gaa act ttt gct acc aac tct tac acc ttc    1728
Ser Gly Lys Tyr Thr Thr Glu Thr Phe Ala Thr Asn Ser Tyr Thr Phe
            565             570                 575

tcc tac att gcc cag gaa taa                                        1749
Ser Tyr Ile Ala Gln Glu  *
            580
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<210> 33
<211> 582
<212> PRT
<213> Adenovirus serotype 2 fiber

<400> 33
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Arg Val Ser Glu Pro Leu Asp Thr Ser His Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Ser Gly Leu Thr Leu Asp Lys Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95
Ile Ser Leu Asp Thr Ser Ala Pro Leu Thr Ile Thr Ser Gly Ala Leu
            100                 105                 110
Thr Val Ala Thr Thr Ala Pro Leu Ile Val Thr Ser Gly Ala Leu Ser
        115                 120                 125
Val Gln Ser Gln Ala Pro Leu Thr Val Gln Asp Ser Lys Leu Ser Ile
    130                 135                 140
Ala Thr Lys Gly Pro Ile Thr Val Ser Asp Gly Lys Leu Ala Leu Gln
145                 150                 155                 160
Thr Ser Ala Pro Leu Ser Gly Ser Asp Ser Asp Thr Leu Thr Val Thr
                165                 170                 175
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asn Met
            180                 185                 190
Glu Asp Pro Ile Tyr Val Asn Asn Gly Lys Ile Gly Ile Lys Ile Ser
```

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              195                    200                    205
Gly Pro Leu Gln Val Ala Gln Asn Ser Asp Thr Leu Thr Val Val Thr
    210                    215                    220
Gly Pro Gly Val Thr Val Glu Gln Asn Ser Leu Arg Thr Lys Val Ala
225                    230                    235                    240
Gly Ala Ile Gly Tyr Asp Ser Ser Asn Asn Met Glu Ile Lys Thr Gly
                245                    250                    255
Gly Gly Met Arg Ile Asn Asn Asn Leu Leu Ile Leu Asp Val Asp Tyr
            260                    265                    270
Pro Phe Asp Ala Gln Thr Lys Leu Arg Leu Lys Leu Gly Gln Gly Pro
        275                    280                    285
Leu Tyr Ile Asn Ala Ser His Asn Leu Asp Ile Asn Tyr Asn Arg Gly
    290                    295                    300
Leu Tyr Leu Phe Asn Ala Ser Asn Asn Thr Lys Lys Leu Glu Val Ser
305                    310                    315                    320
Ile Lys Lys Ser Ser Gly Leu Asn Phe Asp Asn Thr Ala Ile Ala Ile
                325                    330                    335
Asn Ala Gly Lys Gly Leu Glu Phe Asp Thr Asn Thr Ser Glu Ser Pro
            340                    345                    350
Asp Ile Asn Pro Ile Lys Thr Lys Ile Gly Ser Gly Ile Asp Tyr Asn
        355                    360                    365
Glu Asn Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp
    370                    375                    380
Asn Ser Gly Ala Ile Thr Ile Gly Asn Lys Asn Asp Asp Lys Leu Thr
385                    390                    395                    400
Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile His Ser Asp
                405                    410                    415
Asn Asp Cys Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val
            420                    425                    430
Leu Ala Thr Val Ala Ala Leu Ala Val Ser Gly Asp Leu Ser Ser Met
        435                    440                    445
Thr Gly Thr Val Ala Ser Val Ser Ile Phe Leu Arg Phe Asp Gln Asn
    450                    455                    460
Gly Val Leu Met Glu Asn Ser Ser Leu Lys Lys His Tyr Trp Asn Phe
465                    470                    475                    480
Arg Asn Gly Asn Ser Thr Asn Ala Asn Pro Tyr Thr Asn Ala Val Gly
                485                    490                    495
Phe Met Pro Asn Leu Leu Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala
            500                    505                    510
Lys Asn Asn Ile Val Ser Gln Val Tyr Leu His Gly Asp Lys Thr Lys
        515                    520                    525
Pro Met Ile Leu Thr Ile Thr Leu Asn Gly Thr Ser Glu Ser Thr Glu
    530                    535                    540
Thr Ser Glu Val Ser Thr Tyr Ser Met Ser Phe Thr Trp Ser Trp Glu
545                    550                    555                    560
Ser Gly Lys Tyr Thr Thr Glu Thr Phe Ala Thr Asn Ser Tyr Thr Phe
                565                    570                    575
Ser Tyr Ile Ala Gln Glu
            580
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<210> 34
<211> 1746
<212> DNA
<213> Adenovirus serotype 5 fiber

<220>
<221> CDS
<222> (1)...(1746)

<400> 34

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atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc gtg tat cca    48
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                  10                  15

tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc    96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
             20                  25                  30

ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct   144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
         35                  40                  45

ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc   192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
     50                  55                  60

aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc   240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65              70                  75                  80

caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac   288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                 85                  90                  95

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta   336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100                 105                 110

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc   384
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
            115                 120                 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att   432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
        130                 135                 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa   480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act   528
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            165                 170                 175

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg   576
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
        180                 185                 190

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg   624
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
        195                 200                 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act   672
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210                 215                 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act   720
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                 230                 235                 240

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca   768
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Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                 245             250             255

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt    816
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
             260             265             270

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag    864
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
         275             280             285

ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac    912
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
     290             295             300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag    960
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305             310             315             320

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata   1008
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                 325             330             335

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   1056
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
             340             345             350

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   1104
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
         355             360             365

tca aac aag gct atg gtt cct aaa cta gga act ggc ctt agt ttt gac   1152
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
     370             375             380

agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act   1200
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385             390             395             400

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag   1248
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
                 405             410             415

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata   1296
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
             420             425             430

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata   1344
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
         435             440             445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat   1392
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
     450             455             460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt   1440
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465             470             475             480

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga   1488
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
```

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```
                        485                    490                      495
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc      1536
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
            500                 505                 510

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa      1584
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
            515                 520                 525

cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac      1632
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
        530                 535                 540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc      1680
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545                 550                 555                 560

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca      1728
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
                565                 570                 575

tac att gcc caa gaa taa                                              1746
Tyr Ile Ala Gln Glu *
                580
```

<210> 35
<211> 581
<212> PRT
<213> Adenovirus serotype 5 fiber

<400> 35
```
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5                   10                  15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35                  40                  45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100                 105                 110
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
            115                 120                 125
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130                 135                 140
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                165                 170                 175
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180                 185                 190
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
        195                 200                 205
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210                 215                 220
```

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```
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225             230             235             240
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
            245             250             255
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260             265             270
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
        275             280             285
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
    290             295             300
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305             310             315             320
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
            325             330             335
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
            340             345             350
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
        355             360             365
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
    370             375             380
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385             390             395             400
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
            405             410             415
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
            420             425             430
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
        435             440             445
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
    450             455             460
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
465             470             475             480
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
            485             490             495
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
        500             505             510
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
    515             520             525
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
    530             535             540
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
545             550             555             560
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
            565             570             575
Tyr Ile Ala Gln Glu
            580
```

<210> 36
<211> 1098
<212> DNA
<213> Adenovirus serotype 37 fiber

<220>
<221> CDS
<222> (1)...(1098)

<400> 36
```
atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc    48
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
1               5                   10                  15
```

```
tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt    96
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
             20                  25                  30

gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc   144
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
         35                  40                  45

aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag   192
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
     50                  55                  60

gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct   240
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65                  70                  75                  80

aag gct cca ctg caa gtt aat act gat aaa aaa ctt gag ctt gca tat   288
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
                 85                  90                  95

gat aat cca ttt gaa agt agt gct aat aaa ctt agt tta aaa gta gga   336
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
            100                 105                 110

cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat   384
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
        115                 120                 125

tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa   432
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
    130                 135                 140

aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta   480
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145                 150                 155                 160

aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca   528
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
                165                 170                 175

tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca   576
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
            180                 185                 190

tct cca aac tgc aca att gct caa gat aag gac tct aaa ctc act ttg   624
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
        195                 200                 205

gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att   672
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
    210                 215                 220

gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca aaa   720
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys
225                 230                 235                 240

ata aaa agt ttt act att aaa ctg cta ttt aat aag aac gga gtg ctt   768
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
                245                 250                 255
```

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```
tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga    816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
            260             265             270

aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct    864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
            275             280             285

aat ttg gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga    912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
        290             295             300

gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca    960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
305             310             315             320

gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct   1008
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
                325             330             335

atc aca ttt aac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt   1056
Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
            340             345             350

gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga            1098
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *
            355             360             365
```

```
<210> 37
<211> 365
<212> PRT
<213> Adenovirus serotype 37 fiber

<400> 37
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
  1           5              10              15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
            20              25              30
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
        35              40              45
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
    50              55              60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65              70              75              80
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
            85              90              95
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
            100             105             110
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
        115             120             125
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
        130             135             140
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145             150             155             160
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
            165             170             175
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
        180             185             190
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
```

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```
            195                200                205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
    210                215                220
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Lys
225                230                235                240
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
            245                250                255
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
        260                265                270
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
    275                280                285
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
    290                295                300
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
305                310                315                320
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
            325                330                335
Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
            340                345                350
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
    355                360                365
```

<210> 38
<211> 1098
<212> DNA
<213> Adenovirus serotype 19p fiber

<220>
<221> CDS
<222> (1)...(1098)

<400> 38
```
atg tca aag agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc      48
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
1               5                   10                  15

tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt      96
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
            20                  25                  30

gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg gta ctg tca ctc     144
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
        35                  40                  45

aaa ctg gct gat cca atc acc att acc aat ggg gat gta tcc ctc aag     192
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
    50                  55                  60

gtg gga ggt ggt ctc act ttg caa gat gga agc cta act gta aac cct     240
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65                  70                  75                  80

aag gct cca ctg caa gtt act act gat aaa aaa ctt gag ctt gca tat     288
Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Lys Leu Glu Leu Ala Tyr
            85                  90                  95

gat aat cca ttt gaa tgt agt gct aat aaa ttt agt tta aaa gta gga     336
Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly
        100                 105                 110
```

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```
cat gga tta aaa gta tta gat gaa aaa agt gct gcg ggg tta aaa gat        384
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
        115             120             125

tta att ggc aaa ctt gtg gtt tta aca gga aaa gga ata ggc act gaa        432
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
    130             135             140

aat tta gaa aat aca gat ggt agc agc aga gga att ggt ata aat gta        480
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145             150             155             160

aga gca aga gaa ggg ttg aca ttt gac aat gat gga tac ttg gta gca        528
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
            165             170             175

tgg aac cca aag tat gac acg cgc aca ctt tgg aca aca cca gac aca        576
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
        180             185             190

tct cca aac tgc aca att gct cag gat aag gac tct aaa ctc act ttg        624
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
        195             200             205

gta ctt aca aag tgt gga agt caa ata tta gct aat gtg tct ttg att        672
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
    210             215             220

gtg gtc gca gga aag tac cac atc ata aat aat aag aca aat cca gaa        720
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu
225             230             235             240

ata aaa agt ttt act att aaa ctg tta ttt aat aag aac gga gtg ctt        768
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
            245             250             255

tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga        816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
        260             265             270

aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct        864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
        275             280             285

aat tta gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga        912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
    290             295             300

gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca        960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
305             310             315             320

gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct       1008
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
            325             330             335

atc aca ttt gac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt       1056
Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
            340             345             350

gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga              1098
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu ***
```

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```
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu  *
        355             360             365
```

<210> 39
<211> 365
<212> PRT
<213> Adenovirus serotype 19p fiber

<400> 39

```
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
1               5               10              15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
            20              25              30
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
        35              40              45
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
    50              55              60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65              70              75              80
Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Lys Leu Glu Leu Ala Tyr
            85              90              95
Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly
        100             105             110
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
    115             120             125
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
    130             135             140
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145             150             155             160
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
            165             170             175
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
        180             185             190
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
    195             200             205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
    210             215             220
Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu
225             230             235             240
Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
            245             250             255
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
        260             265             270
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
    275             280             285
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
    290             295             300
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
305             310             315             320
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
            325             330             335
Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
        340             345             350
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
    355             360             365
```

<210> 40
<211> 1228

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```
<212> DNA
<213> Adenovirus serotype 9 fiber

<220>
<221> CDS
<222> (50)...(1138)

<400> 40
aagggatgtc aaattcctgg tccacaattt tcattgtctt ccctctcag atg tca aag    58
                                                        Met Ser Lys
                                                          1

agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc tat. ggc tac   106
Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro Tyr Gly Tyr
      5                  10                  15

gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt gtc tcc tcc   154
Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser
 20                  25                  30                  35

gat gga ttc caa aac ttc ccc cct ggg gtc ctg tca ctc aaa cta gct   202
Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala
                     40                  45                  50

gac cca ata gcc atc gtc aat ggg aat gtc tca ctc aaa gtg gga ggg   250
Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys Val Gly Gly
                 55                  60                  65

ggt ctc act ttg caa gat gga act gga aaa cta aca gtc aat gct gat   298
Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val Asn Ala Asp
             70                  75                  80

cca cct ttg caa ctt aca aac aac aaa tta ggg att gct ttg gac gct   346
Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala Leu Asp Ala
         85                  90                  95

cca ttt gat gtt ata gat aat aaa ctc aca ttg tta gcg ggc cat ggc   394
Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala Gly His Gly
100                 105                 110                 115

ttg tct att ata aca aaa gaa aca tca aca ctg cct ggc ttg agg aat   442
Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly Leu Arg Asn
                120                 125                 130

act ctt gta gta tta act gga aag ggt att gga aca gaa tca aca gat   490
Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Ser Thr Asp
            135                 140                 145

aat ggc gga acg gta tgt gtt aga gtt gga gaa ggt ggc ggc tta tca   538
Asn Gly Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly Gly Leu Ser
        150                 155                 160

ttt aat aat gat gga gac ttg gta gca ttt aat aaa aaa gaa gat aag   586
Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys Glu Asp Lys
    165                 170                 175 .

cgc acc cta tgg aca act cca gac aca tct cca aat tgc aag att gat   634
Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Lys Ile Asp
180                 185                 190                 195

cag gat aag gac tct aag tta act ctg gtc ctt aca aag tgt gga agt   682
```

```
Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser
                200                 205                 210

caa ata ttg gct aat gtg tca tta att gtc gta gat ggt aag tac aaa    730
Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Asp Gly Lys Tyr Lys
            215                 220                 225

att atc aat aac aat act caa cca gct ctc aaa gga ttt acc att aaa    778
Ile Ile Asn Asn Asn Thr Gln Pro Ala Leu Lys Gly Phe Thr Ile Lys
            230                 235                 240

tta ttg ttt gat gaa aat gga gta ctt atg gaa tct tca aat ctt ggt    826
Leu Leu Phe Asp Glu Asn Gly Val Leu Met Glu Ser Ser Asn Leu Gly
        245                 250                 255

aaa tca tat tgg aac ttt aga aat gaa aat tca att atg tca aca gct    874
Lys Ser Tyr Trp Asn Phe Arg Asn Glu Asn Ser Ile Met Ser Thr Ala
260                 265                 270                 275

tat gaa aaa gct att gga ttc atg cct aat ttg gta gcc tat cca aaa    922
Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys
                280                 285                 290

cct acc gct ggc tct aaa aaa tat gca aga gat ata gtt tat gga aac    970
Pro Thr Ala Gly Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Asn
            295                 300                 305

atc tac ctt ggt gga aag cca gat caa cca gta acc att aaa act acc    1018
Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Val Thr Ile Lys Thr Thr
            310                 315                 320

ttt aat cag gaa act gga tgt gaa tat tct atc aca ttt gat ttt agt    1066
Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asp Phe Ser
        325                 330                 335

tgg gcc aag act tat gta aat gtt gaa ttt gaa aca acc tct ttt acc    1114
Trp Ala Lys Thr Tyr Val Asn Val Glu Phe Glu Thr Thr Ser Phe Thr
340                 345                 350                 355

ttt tcc tat atc gcc caa gaa tga aagaccaata aacgtgtttt tcatttcaaa   1168
Phe Ser Tyr Ile Ala Gln Glu  *
                360

attttcatgt atctttattg atttttacac cagcacgggt agtcagtctc ccaccaccag  1228
```

```
<210> 41
<211> 362
<212> PRT
<213> Adenovirus serotype 9 fiber

<400> 41
Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
            20                  25                  30
Val Ser Ser Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu
        35                  40                  45
Lys Leu Ala Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys
    50                  55                  60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val
```

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```
65                          70                          75                          80
Asn Ala Asp Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala
                        85                          90                          95
Leu Asp Ala Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala
                    100                         105                         110
Gly His Gly Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly
                    115                         120                         125
Leu Arg Asn Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
        130                         135                         140
Ser Thr Asp Asn Gly Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly
145                         150                         155                         160
Gly Leu Ser Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys
                    165                         170                         175
Glu Asp Lys Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys
                180                         185                         190
Lys Ile Asp Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys
            195                         200                         205
Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Asp Gly
    210                         215                         220
Lys Tyr Lys Ile Ile Asn Asn Asn Thr Gln Pro Ala Leu Lys Gly Phe
225                         230                         235                         240
Thr Ile Lys Leu Leu Phe Asp Glu Asn Gly Val Leu Met Glu Ser Ser
                    245                         250                         255
Asn Leu Gly Lys Ser Tyr Trp Asn Phe Arg Asn Glu Asn Ser Ile Met
                260                         265                         270
Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala
            275                         280                         285
Tyr Pro Lys Pro Thr Ala Gly Ser Lys Lys Tyr Ala Arg Asp Ile Val
    290                         295                         300
Tyr Gly Asn Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Val Thr Ile
305                         310                         315                         320
Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe
                    325                         330                         335
Asp Phe Ser Trp Ala Lys Thr Tyr Val Asn Val Glu Phe Glu Thr Thr
                340                         345                         350
Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
            355                         360
```

```
<210> 42
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad2   third repeat

<400> 42
Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys
  1               5                   10                  15
Lys Thr Lys Ser
            20


<210> 43
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5   third repeat
```

```
<400> 43
Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys
 1               5                   10                  15
Lys Thr Lys Ser
            20


<210> 44
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Repeat motif

<221> VARIANT
<222> 4
<223> Xaa = Thr or Ser

<400> 44
Thr Thr Val Xaa
 1


<210> 45
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Repeat Consensus Sequence

<221> VARIANT
<222> 3,5,7,13
<223> Xaa = Hydrophobic Amino Acid

<221> VARIANT
<222> 1, 2, 4,  6, 8, 9, 11, 12, 14, 15
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 10
<223> Xaa = Pro or Gly

<400> 45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                   10                  15


<210> 46
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad2 21st repeat

<400> 46
Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp Asn Ser
 1               5                   10                  15
```

```
<210> 47
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5 21st repeat

<400> 47
Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp Ser Thr
1               5                   10                  15


<210> 48
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37 last repeat

<400> 48
Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp
1               5                   10                  15


<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Last repeat consensus sequence

<221> VARIANT
<222> 4,7
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 9
<223> Xaa = Asp or Asn

<400> 49
Lys Leu Gly Xaa Gly Leu Xaa Phe Xaa
1               5


<210> 50
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5Ds fiber

<221> CDS
<222> (13)...(1092)

<221> misc_feature
<222> 1130, 1157
<223> n = A,T,C or G
```

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<400> 50
atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
               Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
               1   5   10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt   99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
    15   20   25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg   147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
30   35   40   45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg   195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
                50   55   60

ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac   243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn
            65   70   75

ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc   291
Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr
            80   85   90

aag aaa aag ctt gaa gtt aac cta agc act gcc aag ggg ttg atg ttt   339
Lys Lys Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe
        95   100   105

gac gct aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt   387
Asp Ala Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly
110   115   120   125

tca cct aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat   435
Ser Pro Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His
                130   135   140

ggc cta gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act   483
Gly Leu Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr
            145   150   155

ggc ctt agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat   531
Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn
            160   165   170

aat gat aag cta act ttg tgg acc aca cca gct cca tct cct aac tgt   579
Asn Asp Lys Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys
        175   180   185

aga cta aat gca gag aaa gat gct aaa ctc act ttg gtc tta aca aaa   627
Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys
190   195   200   205

tgt ggc agt caa ata ctt gct aca gtt tca gtt ttg gct gtt aaa ggc   675
Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly
                210   215   220

agt ttg gct cca ata tct gga aca gtt caa agt gct cat ctt att ata   723
Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile
            225   230   235

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```
aga ttt gac gaa aat gga gtg cta cta aac aat tcc ttc ctg gac cca   771
Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro
        240             245                 250

gaa tat tgg aac ttt aga aat gga gat ctt act gaa ggc aca gcc tat   819
Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr
    255             260                 265

aca aac gct gtt gga ttt atg cct aac cta tca gct tat cca aaa tct   867
Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser
270             275                 280                 285

cac ggt aaa act gcc aaa agt aac att gtc agt caa gtt tac tta aac   915
His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn
            290                 295                 300

gga gac aaa act aaa cct gta aca cta acc att aca cta aac ggt aca   963
Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr
        305             310                 315

cag gaa aca gga gac aca act cca agt gca tac tct atg tca ttt tca  1011
Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser
        320             325                 330

tgg gac tgg tct ggc cac aac tac att aat gaa ata ttt gcc aca tcc  1059
Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser
        335             340                 345

tct tac act ttt tca tac att gcc caa gaa taa agaagcggcc gcgttatgaa 1112
Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu  *
350             355

gggcgaattc cagcacantg gcggccgtta ttagtggatc cgagntcatg ca         1164
```

```
<210> 51
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5deltas

<400> 51
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1               5               10                  15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20              25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35              40                  45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50              55                  60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65              70              75                  80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Lys Lys
                85              90                  95
Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr
            100             105                 110
Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn
    115             120                 125
Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu
130             135                 140
```

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```
Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser
145                 150                 155                 160
Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys
                165                 170                 175
Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn
                180                 185                 190
Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser
            195                 200                 205
Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala
    210                 215                 220
Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp
225                 230                 235                 240
Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp
                245                 250                 255
Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala
            260                 265                 270
Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys
        275                 280                 285
Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys
    290                 295                 300
Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr
305                 310                 315                 320
Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp
                325                 330                 335
Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr
            340                 345                 350
Phe Ser Tyr Ile Ala Gln Glu
            355
```

```
<210> 52
<211> 1920
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37k fiber

<221> CDS
<222> (13)...(1755)

<221> misc_feature
<222> 1867, 1875
<223> n = A,T,C or G

<400> 52
gcaagatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc    51
           Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
            1               5                   10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt     99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
     15                  20                  25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg    147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
 30                  35                  40                  45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg    195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
                 50                  55                  60
```

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```
ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn   243
              65           70                    75

ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc
Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr   291
          80                    85                    90

aag tca aac ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca
Lys Ser Asn Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser   339
          95                   100                   105

gaa gcc cta act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac
Glu Ala Leu Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn       387
110                   115                   120               125

aca ctc acc atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa
Thr Leu Thr Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys   435
              130                   135                   140

ctt agc att gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta
Leu Ser Ile Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu   483
              145                   150                   155

gcc ctg caa aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt
Ala Leu Gln Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu   531
          160                   165                   170

act atc act gcc tca ccc cct cta act act gcc act ggt agc ttg ggc
Thr Ile Thr Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly   579
          175                   180                   185

att gac ttg aaa gag ccc att tat aca caa aat gga aaa cta gga cta
Ile Asp Leu Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu   627
190                   195                   200                   205

aag tac ggg gct cct ttg cat gta aca gac gac cta aac act ttg acc
Lys Tyr Gly Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr   675
              210                   215                   220

gta gca act ggt cca ggt gtg act att aat aat act tcc ttg caa act
Val Ala Thr Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr   723
          225                   230                   235

aaa gtt act gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt
Lys Val Thr Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu   771
          240                   245                   250

aat gta gca gga gga cta agg att gat tct caa aac aga cgc ctt ata
Asn Val Ala Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile   819
255                   260                   265

ctt gat gtt agt tat ccg ttt gat gct caa aac caa cta aat cta aga
Leu Asp Val Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg   867
270                   275                   280               285

cta gga cag ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att
Leu Gly Gln Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile   915
              290                   295                   300
```

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```
aac tac aac aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa
Asn Tyr Asn Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys      963
            305                 310                 315

aag ctt gag gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct
Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala     1011
            320                 325                 330

aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct
Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro     1059
            335                 340                 345

aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta
Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu     1107
350                 355                 360                 365

gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act ggc ctt
Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu     1155
                370                 375                 380

agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat aat gat
Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp     1203
            385                 390                 395

aag cta act ttg tgg acc aca cca gac act agt cca aac tgc aca att
Lys Leu Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile     1251
            400                 405                 410

gct caa gat aag gac tct aaa ctc act ttg gta ctt aca aag tgt gga
Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly     1299
            415                 420                 425

agt caa ata tta gct aat gtg tct ttg att gtg gtc gca gga aag tac
Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr     1347
430                 435                 440                 445

cac atc ata aat aat aag aca aat cca aaa ata aaa agt ttt act att
His Ile Ile Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile     1395
                450                 455                 460

aaa ctg cta ttt aat aag aac gga gtg ctt tta gac aac tca aat ctt
Lys Leu Leu Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu     1443
            465                 470                 475

gga aaa gct tat tgg aac ttt aga agt gga aat tcc aat gtt tcg aca
Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr     1491
            480                 485                 490

gct tat gaa aaa gca att ggt ttt atg cct aat ttg gta gcg tat cca
Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro     1539
            495                 500                 505

aaa ccc agt aat tct aaa aaa tat gca aga gac ata gtt tat gga act
Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr     1587
510                 515                 520                 525

ata tat ctt ggt gga aaa cct gat cag cca gca gtc att aaa act acc
Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr     1635
                530                 535                 540

ttt aac caa gaa act gga tgt gaa tac tct atc aca ttt aac ttt agt
Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser     1683
```

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```
Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser
            545                 550                 555

tgg tcc aaa acc tat gaa aat gtt gaa ttt gaa acc acc tct ttt acc   1731
Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr
        560                 565                 570

ttc tcc tat att gcc caa gaa tga aaaagcggcc gctcgagtct agagggcccg   1785
Phe Ser Tyr Ile Ala Gln Glu  *
    575                 580

tttaaacccg ctgatcagcc tcgactgtgc cttctagttg ccagccatct gttgtttgcc   1845
cctccccgt gccttccttg ancctggaan gtgccactcc cactgtcctt tcctaataaa   1905
atgaggaaat gcatc                                                    1920
                                                                    1920
```

<210> 53
<211> 580
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37k

<400> 53
```
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1           5                 10                  15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35                  40                  45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65                  70                  75                  80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
                85                  90                  95
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
            100                 105                 110
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
            115                 120                 125
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
    130                 135                 140
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
145                 150                 155                 160
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
                165                 170                 175
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
            180                 185                 190
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
            195                 200                 205
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
    210                 215                 220
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
225                 230                 235                 240
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                245                 250                 255
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
            260                 265                 270
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
    275                 280                 285
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
```

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```
      290                      295                      300
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
305                      310                      315                      320
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
                     325                      330                      335
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
                 340                      345                      350
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
             355                      360                      365
Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
         370                      375                      380
Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
385                      390                      395                      400
Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile Ala Gln Asp
                     405                      410                      415
Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
                 420                      425                      430
Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr His Ile Ile
             435                      440                      445
Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile Lys Leu Leu
         450                      455                      460
Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu Gly Lys Ala
465                      470                      475                      480
Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr Ala Tyr Glu
                 485                      490                      495
Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys Pro Ser
             500                      505                      510
Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr Ile Tyr Leu
         515                      520                      525
Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr Phe Asn Gln
         530                      535                      540
Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser Trp Ser Lys
545                      550                      555                      560
Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr Phe Ser Tyr
                 565                      570                      575
Ile Ala Gln Glu
                580
```

```
<210> 54
<211> 1767
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37s fiber

<221> CDS
<222> (13)...(1749)

<400> 54
atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc   51
              Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
               1               5                       10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt     99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
 15                      20                      25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg    147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
```

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```
    30                      35                          40                              45
gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg    195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
                    50                  55                  60

ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc agc    243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser
                65                  70                  75

cta act gta aac cct aag gct cca ctg caa gtt aat act gat tca aac    291
Leu Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn
            80                  85                  90

ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta    339
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
        95                  100                 105

act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc    387
Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
110                 115                 120                 125

atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att    435
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
                130                 135                 140

gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa    483
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
                145                 150                 155

aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act    531
Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
            160                 165                 170

gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg    579
Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
        175                 180                 185

aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg    627
Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
190                 195                 200                 205

gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act    675
Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
                210                 215                 220

ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act    723
Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
                225                 230                 235

gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca    771
Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
                240                 245                 250

gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt    819
Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
        255                 260                 265

agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag    867
Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
270                 275                 280                 285
```

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```
ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac    915
Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
            290             295                     300

aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag    963
Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
            305                     310                     315

gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct aca gcc ata   1011
Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
            320                     325             330

gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca   1059
Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
        335                     340                 345

aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta gaa ttt gat   1107
Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
350                     355                     360             365

tca aac att ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac   1155
Ser Asn Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp
                370                     375                 380

aat gat ggt gcc att aca gta gga aac aaa aat aat gat aag cta act   1203
Asn Asp Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
                385                     390                     395

ttg tgg acc aca cca gct cca tct cct aac tgt aga cta aat gca gag   1251
Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
            400                     405                     410

aaa gat gct aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata   1299
Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
    415                     420                     425

ctt gct aca gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata   1347
Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
430                     435                     440                 445

tct gga aca gtt caa agt gct cat ctt att ata aga ttt gac gaa aat   1395
Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
                450                     455                     460

gga gtg cta cta aac aat tcc ttc ctg gac cca gaa tat tgg aac ttt   1443
Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
            465                     470                     475

aga aat gga gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga   1491
Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
            480                     485                     490

ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc   1539
Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
    495                     500                     505

aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa   1587
Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
510                     515                     520                 525
```

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```
cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac    1635
Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
            530             535             540

aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc    1683
Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
            545             550             555

cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca    1731
His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
            560             565             570

tac att gcc caa gaa taa agaagcggcc gcgttatg                        1767
Tyr Ile Ala Gln Glu *
        575
```

<210> 55
<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5s/Ad37s

<400> 55

```
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
            35                  40                  45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Ser Leu Thr Val
65                  70                  75                  80
Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Ser Asn Ile Asn Leu
                85                  90                  95
Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu Thr Val Ala
                100                 105                 110
Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr Met Gln Ser
            115                 120                 125
Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile Ala Thr Gln
    130                 135                 140
Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln Thr Ser Gly
145                 150                 155                 160
Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr Ala Ser Pro
                165                 170                 175
Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu Lys Glu Pro
                180                 185                 190
Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly Ala Pro Leu
        195                 200                 205
His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr Gly Pro Gly
    210                 215                 220
Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr Gly Ala Leu
225                 230                 235                 240
Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala Gly Gly Leu
                245                 250                 255
Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val Ser Tyr Pro
        260                 265                 270
Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln Gly Pro Leu
```

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```
          275                    280                    285
Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn Lys Gly Leu
    290                    295                    300
Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu Val Asn Leu
305                    310                    315                    320
Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile Ala Ile Asn
                325                    330                    335
Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro Asn Thr Asn
            340                    345                    350
Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp Ser Asn Ile
        355                    360                    365
Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly
    370                    375                    380
Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr Leu Trp Thr
385                    390                    395                    400
Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala
                405                    410                    415
Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr
            420                    425                    430
Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
        435                    440                    445
Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu
    450                    455                    460
Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
465                    470                    475                    480
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
                485                    490                    495
Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
            500                    505                    510
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
        515                    520                    525
Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
    530                    535                    540
Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
545                    550                    555                    560
Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
                565                    570                    575
Gln Glu
```

```
<210> 56
<211> 1132
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad37s/Ad5k fiber

<221> CDS
<222> (16)...(1116)

<221> misc_feature
<222> 1125
<223> n = A,T,C or G

<400> 56
gtcgcaagat ccaag atg aag agg gcc cgg ccc agc gaa gat gac ttc aac    51
                  Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn
                  1               5                   10
```

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```
ccc gtc tac ccc tat ggc tac gcg cgg aat cag aat atc ccc ttc ctc    99
Pro Val Tyr Pro Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu
         15            20                25

act ccc ccc ttt gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg   147
Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly
     30            35                40

gta ctg tca ctc aaa ctg gct gat cca atc acc att acc aat ggg gat   195
Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp
 45            50            55                60

gta tcc ctc aag gtg gga ggt ggt ctc act ttg caa gat gga agc cta   243
Val Ser Leu Lys Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu
             65                70                75

act gta aac cct aag gct cca ctg caa gtt aat act gat aaa aaa ctt   291
Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu
             80            85                90

gag ctt gca tat gat aat cca ttt gaa agt agt gct aat aaa ctt agt   339
Glu Leu Ala Tyr Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser
         95            100               105

tta aaa gta gga cat gga tta aaa gta tta gat gaa aaa agt gct gcg   387
Leu Lys Val Gly His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala
     110           115               120

ggg tta aaa gat tta att ggc aaa ctt gtg gtt tta aca gga aaa gga   435
Gly Leu Lys Asp Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly
125           130               135               140

ata ggc act gaa aat tta gaa aat aca gat ggt agc agc aga gga att   483
Ile Gly Thr Glu Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile
             145               150               155

ggt ata aat gta aga gca aga gaa ggg ttg aca ttt gac aat gat gga   531
Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly
             160               165               170

tac ttg gta gca tgg aac cca aag tat gac acg cgc act ttg tgg acc   579
Tyr Leu Val Ala Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr
         175               180               185

aca cca gct cca tct cct aac tgt aga cta aat gca gag aaa gat gct   627
Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala
     190               195               200

aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata ctt gct aca   675
Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr
205               210               215               220

gtt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata tct gga aca   723
Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
             225               230               235

gtt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg cta   771
Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu
             240               245               250

cta aac aat tcc ttc ctg gat cca gaa tat tgg aac ttt aga aat gga   819
Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
```

```
Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
        255             260             265

gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg cct   867
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
    270             275             280

aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt aac   915
Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
285             290             295             300

att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta aca   963
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
            305             310             315

cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act cca  1011
Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
            320             325             330

agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac tac  1059
Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
            335             340             345

att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att gcc  1107
Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
            350             355             360

caa gaa taa agaagcggnc gctcga                                     1132
Gln Glu *
365
```

```
<210> 57
<211> 366
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37s/Ad5k

<400> 57
Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn Pro Val Tyr Pro
1           5               10              15
Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
            20              25              30
Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
        35              40              45
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
    50              55              60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
65              70              75              80
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
            85              90              95
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
            100             105             110
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
        115             120             125
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
    130             135             140
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145             150             155             160
```

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Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
                    165   170   175
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Ala Pro
            180   185   190
Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Leu
        195   200   205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu
    210   215   220
Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala
225   230   235   240
His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser
                245   250   255
Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu
            260   265   270
Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala
        275   280   285
Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln
290   295   300
Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr
305   310   315   320
Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser
                325   330   335
Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile
            340   345   350
Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu
        355   360   365

<210> 58
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37 third repeat

<400> 58
Gly Ser Leu Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp
1   5   10   .   15

<210> 59
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad8 last repeat

<400> 59
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Asp Asn
1   5   10

<210> 60
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad9 last repeat

```
<400> 60
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Asn Asp .
 1               5                   10


<210> 61
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad15 last repeat

<400> 61
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Glu Ala
 1               5                   10


<210> 62
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Penton region

<400> 62
His Ala Ile Arg Gly Asp Thr Phe
 1               5


<210> 63
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Penton amino acid replacement

<400> 63
Ser Arg Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Ser
 1               5                   10                  15


<210> 64
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Fiber protein conserved sequence

<400> 64
Thr Trp Leu Thr
 1


<210> 65
<211> 4
<212> PRT
<213> Artificial Sequence
```

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```
<220>
<223> HSP binding motif

<400> 65
Lys Lys Thr Lys
 1


<210> 66
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad8 third repeat

<400> 66
Gly Lys Leu Thr Val Asn Thr Glu Pro Pro Leu His Leu Thr Asn Asn
 1               5                  10                      15


<210> 67
<211> 16
<212> PRT
<213> Artificial Sequence

<220>   .
<223> Ad9 third repeat

<400> 67
Gly Lys Leu Thr Val Asn Ala Asp Pro Pro Leu Gln Leu Thr Asn Asn
 1               5                  10                      15


<210> 68
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad15 third repeat

<400> 68
Gly Asn Leu Thr Val Asn Thr Glu Pro Pro Leu Gln Leu Thr Asn Asn
 1               5                  10                      15


<210> 69
<211> 3929
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector pCR2.1

<400> 69
agcgcccaat acgcaaaccg cctctccccg cgcgttggcc gattcattaa tgcagctggc 60
acgacaggtt tcccgactgg aaagcgggca gtgagcgcaa cgcaattaat gtgagttagc 120
tcactcatta ggcacccccag gctttacact ttatgcttcc ggctcgtatg ttgtgtggaa 180
ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac gccaagcttg 240
gtaccgagct cggatccact agtaacggcc gccagtgtgc tggaattcgg cttaagccga 300
```

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```
attctgcaga tatccatcac actggcggcc gctcgagcat gcatctagag ggcccaattc 360
gccctatagt gagtcgtatt acaattcact ggccgtcgtt ttacaacgtc gtgactggga 420
aaaccctggc gttacccaac ttaatcgcct tgcagcacat cccccttttcg ccagctggcg 480
taatagcgaa gaggcccgca ccgatcgccc ttcccaacag ttgcgcagcc tgaatggcga 540
atggacgcgc cctgtagcgg cgcattaagc gcggcgggtg tggtggttac gcgcagcgtg 600
accgctacac ttgccagcgc cctagcgccc gctcctttcg ctttcttccc ttcctttctc 660
tttagtgctt tacggcacct cgacccccaaa ctaaatcggg ggctcccttt agggttccga 720
gggccatcgc cctgatagac ggttttttcgc cctttgacgt agggtgatgg ttcacgtagt 780
agtggactct tgttccaaac tggaacaaca ctcaaccctaa tctcggtcta ttcttttgat 840
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